Vezf1: 1 to 3640

```
CGGGGGGAGTGGGGAGGAGGGGG[illegible]CCGCCGCAGCCATGGAGGCCAACTGGACCGCGTTCCTGTTCCAG[illegible]ACGAAGCATCCCAT     90
                                                    M  E  A  N  W  T  A  F  L  F  Q  A  H  E  A  S  H  17

CACCAACAGCAGGCAGCGCAGAACAGCTTGCTGCCCCTCCTGAGTTCTGCTGTGGAGCCCCCTGATCAGAAACCGTTGCTTCCAATACCA     180
 H  Q  Q  Q  A  A  Q  N  S  L  L  P  L  L  S  S  A  V  E  P  P  D  Q  K  P  L  L  P  I  P  47

ATTACTCAGAAACCTCAGGCTGCACCAGAAACATTAAAGGATGCCATTGGGATTAAAAAAGAAAAACCCAAAACTTCGTTTGTGTGCACT     270
 I  T  Q  K  P  Q  A  A  P  E  T  L  K  D  A  I  G  I  K  K  E  K  P  K  T  S  F  V  C  T  77

TACTGCAGTAAAGCATTCAGGGACAGCTATCACCTGAGGCGCCATCAGTCCTGCCACACAGGGATCAAGTTGGTGTCTCGGGCAAAGAAA     360
 Y  C  S  K  A  F  R  D  S  Y  H  L  R  R  H  Q  S  C  H  T  G  I  K  L  V  S  R  A  K  K  107

ACCCCCACCACGGTGGTTCCCCTTATCTCCACCATTGCTGGGGACAGCAGCCGAACTTCGTTGGTTTCAACTATTGCAGGCATCTTGTCA     450
 T  P  T  T  V  V  P  L  I  S  T  I  A  G  D  S  S  R  T  S  L  V  S  T  I  A  G  I  L  S  137

ACAGTCACTACATCTTCCTCGGGCACCAACCCCAGCAGCAGCGCTAGTACCACAGCAATGCCTGTGCCCCAGTCTGTCAAGAAACCCAGT     540
 T  V  T  T  S  S  S  G  T  N  P  S  S  S  A  S  T  T  A  M  P  V  P  Q  S  V  K  K  P  S  167

AAGCCTGTCAAGAAGAACCACGCCTGTGAGATGTGTGGGAAGGCCTTCCGGGATGTGTACCACCTCAATCGGCACAAGCTCTCCCATTCG     630
 K  P  V  K  K  N  H  A  C  E  M  C  G  K  A  F  R  D  V  Y  H  L  N  R  H  K  L  S  H  S  197

GACGAAAAGCCCTTTGAGTGTCCTATTTGTAATCAGCGCTTCAAGAGGAAGGACCGGATGACTTACCATGTGAGGTCTCATGAAGGAGGC     720
 D  E  K  P  F  E  C  P  I  C  N  Q  R  F  K  R  K  D  R  M  T  Y  H  V  R  S  H  E  G  G  227

ATCACCAAACCCTATACTTGCAGTGTTTGTGGGAAAGGCTTCTCAAGGCCTGACCACCTAAGCTGTCATGTAAAACATGTGCATTCAACA     810
 I  T  K  P  Y  T  C  S  V  C  G  K  G  F  S  R  P  D  H  L  S  C  H  V  K  H  V  H  S  T  257

GAAAGACCCTTCAAATGCCAAACGTGCACTGCTGCCTTTGCCACCAAAGACAGACTACGGACACACATGGTGCGCCACGAAGGCAAGGTA     900
 E  R  P  F  K  C  Q  T  C  T  A  A  F  A  T  K  D  R  L  R  T  H  M  V  R  H  E  G  K  V  287

TCATGTAACATCTGTGGGAAGCTCTTGAGTGCAGCATATATCACCAGCCACTTAAAGACACATGGGCAGAGCCAAAGTATCAACTGTAAC     990
 S  C  N  I  C  G  K  L  L  S  A  A  Y  I  T  S  H  L  K  T  H  G  Q  S  Q  S  I  N  C  N  317

ACGTGCAAACAAGGCATCAGCAAAACGTGCATGAGTGAGGAGACCAGCAATCAGAAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAG     1080
 T  C  K  Q  G  I  S  K  T  C  M  S  E  E  T  S  N  Q  K  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  347
                                                    *     *  *  *  *  *  *  *  *  *  *  *

CAACAACAACAACATGTGACAAGCTGGCCAGGGAAGCAGGTAGAGACACTGAGACTGTGGGAAGAAGCTGTCAAAGCAAGAAAGAAAGAA     1170
 Q  Q  Q  Q  H  V  T  S  W  P  G  K  Q  V  E  T  L  R  L  W  E  E  A  V  K  A  R  K  K  E  377
 *  *  *  *

GCTGCCAACCTGTGCCAAACCTCCACGGCTGCTACGACACCAGTGACTCTCACTACTCCATTCAATATAACGTCCTCTGTGTCGTCTGGG     1260
 A  A  N  L  C  Q  T  S  T  A  A  T  T  P  V  T  L  T  T  P  F  N  I  T  S  S  V  S  S  G  407

ACTATGTCAAACCCAGTCACAGTGGCAGCTGCAATGAGCATGAGAAGTCCAGTAAATGTCTCAAGTGCAGTTAACATAACCAGCCCCTTA     1350
 T  M  S  N  P  V  T  V  A  A  A  M  S  M  R  S  P  V  N  V  S  S  A  V  N  I  T  S  P  L  437

GCCATGACCTCACCTTTAACACTCACCACCCCAGTCAACCTCCCCACCCCTGTGACCGCCCCAGTGAATATAGCACACCCTGTCACCATC     1440
 A  M  T  S  P  L  T  L  T  T  P  V  N  L  P  T  P  V  T  A  P  V  N  I  A  H  P  V  T  I  467

ACATCTCCAATGAACCTGCCCACTCCTATGACATTAGCTGCCCCTCTCAATATAGCAATGAGGCCTGTAGAAAGTATGCCTTTCTTGCCC     1530
 T  S  P  M  N  L  P  T  P  M  T  L  A  A  P  L  N  I  A  M  R  P  V  E  S  M  P  F  L  P  497

CAAGCTTTGCCTACGTCACCGCCTTGGTAAACAGTATTATAAGTCAAAATTGGGTTAAAGTAAATATTTACCAGCAACTTAACCTTAGTT     1620
 Q  A  L  P  T  S  P  P  W                                                                 506

GATTAAAGCAAAAAGCAGACTATGAAATTGGGAGGTTTTATTATGTTAGTTAATAAGAGTGTAGTAGCTCCAATTTTGCTGGGGTTGTTC     1710
AAAGTAGGGTATATGTGTAACTTATCACTGGACCACTTTAGTTTACTCAGAAACCCCTTTAGCTGACACCATTGCTTAAACAGGATAGTA     1800
GCTGGCAAGACGAAATGCCAGAATTAAAACCAATCATAAAACCCATTTCAAAATAAAAAAGCATTATTTGTTTTTATTATTATTTTTAAT     1890
ACAACAGAATCATTTTATTGTAAACACTAGCAGAGTTCTTCCCTCTGTACAAGGTGGACGGTTTTAACCTGGAGCTCAAGCCCACAGACT     1980
GAGAGCTAGTGTAGCATTGTCTGTGGTTTTGCTCGTATGAGTGAACAGAGGCATTGTCATAATAAAATGCATTTCAGAGAATATGCATTT     2070
TACCTTTGGGAATATGTTAATTTCAGGCAGCATTCCCTATGGGAAAGGTGATACCAGCTCTGATATGCAAAGCATATGATAATTTATCAT     2160
TCTAACTTCAACATATAATAGGGATTGTGACCTGATATTTGGAGATGTAAATATTGCTCAGCATATTAATCCCTGATGGAATATAGCATT     2250
GTAGTTGACTTTTTAAAAAAAAAAAAACAAAAAAAAAAAAAAAGGAATTCCGAGAGCTGTCACTGCCTTTGAATGCTATCCCTGGGATAGG     2340
GGTGGCTTCAGAACCCAGGAAGTGGCCAAGGGGCACAGACTCTGCTGGAGGCCTGAGCCGGGGGTTCCATAGGAGACTGACAGGAGACAT     2430
TTTGCCTTAGGCCACAAAAAGAAGAAGGCTACCCCACTTACAGATGCAGACCATGTGGGGCTCCGGAGAACTGCTTGTAGCATGGTTTCT     2520
AGTGTTGGCAGCAGATGGTACTACTGAGCATGTCTACAGACCCAGTCGTAGAGTGTGTACTGTGGGGATTTCCGGAGGTTCCATCTCGGA     2610
GACCTTTGTGCAGCGTGTATACCAGCCTTACCTCACCACTTGCGACGGACACAGAGCCTGCAGCACCTACCGAACCATCTACCGGACTGC     2700
CTATCGCCGTAGCCCTGGGGTGACTCCCGCAAGGCCTCGCTATGCTTGCTGCCCTGGTTGGAAGAGGACCAGTGGGCTCCCTGGGGCTTG     2790
TGGAGCAGCAATATGCCAGCCTCCATGTGGGAATGGAGGGAGTTCATCCGCCCAGGACACTGCCGCTGCCCTGTGGATGGCAGGGAGATA     2880
CTTGCCAGACAGATGTTGATGAATGCAGTACAGGAGAGGCCAGTTGTCCCCAGCGCTGTGTCAATACTGTGGGAAGTTACTGGTGCCAGG     2970
GATGGAGGGACAAAGCCCATCTGCAGATGGACCCCCTGCCTGTCTAAGGAGGGGCCCTCCCCTTTCCCCCCAAACCCCACAGCAGGAG     3060
TGGACAGCATGGCGAGAGAGGAGGTGTACAGGCTGCAGGCTCGGGTTGATGTGCTAGAACAGAAACTGCAGTTGGTGCTGGCCCCACTGC     3150
ACAGCCTGGCCTCTCGGTCCACAGAGCATGGGCTACAAGATCCTGGCAGCCTGCTGGTGTCCTTCTTGGAGGAACATCTGGGGTCCTGTG     3240
AGTCCCACAAGACACCACTCCACCCACAGAGAGCCTAGGGGACCCATGGGGTGGACACCAGGGCTGGGTGGATGGAACTTCTTCTGGGAT     3330
GGGCAGATTTGCAAGTTTACACCTTTTTCCTCTCCTGCCCTAGGCTCCTGCAAAAAAGATCTGTGATAACCTCTCACCACCAGGCTGGA     3420
TAGAGCAGTATCCAGATCCCTTGTAGCCAGAGTTCAGGGACGCTGTCTGGTGGTGCCTATGAGCAGAAGCCCTGCCTCATTGTCCCTCTT     3510
TCTTAGGAGGTTCCTAGGACTTGGGTATGGGAGTGGGGTCTTGTGTGACTCTTCAGTGGGGCTCCCTGTCTAAGTGGTAAGGTGGGGAT     3600
TGTCTCCATCTTTGTCATAATAAAGCTGAGACTTGAAAAAAAAAA                                                3645
```

FIGURE 1.

FIGURE 2.

Human DB1 DNA and Protein S q nces:

```
        10         20         30         40         50         60
AGCGGGGGGGAGTGGGGAGGAGGGGGGTCGGCCGCCGCAGCCATGGAGGCCAACTGGACCG
                                              M  E  A  N  W  T>

        70         80         90        100        110        120
CGTTCCTGTTCCAGGCCCATGAAGCTTCCCATCACCAACAGCAGGCAGCACAGAACAGCT
A  F  L  F  Q  A  H  E  A  S  H  H  Q  Q  Q  A  A  Q  N  S>

       130        140        150        160        170        180
TGCTGCCCCTCCTGAGCTCTGCCGTGGAGCCCCCTGATCAGAAACCATTGCTTCCAATAC
L  L  P  L  L  S  S  A  V  E  P  P  D  Q  K  P  L  L  P  I>

       190        200        210        220        230        240
CAATAACTCAGAAACCTCAGGGTGCACCAGAAACATTAAAGGATGCCATTGGGATTAAAA
P  I  T  Q  K  P  Q  G  A  P  E  T  L  K  D  A  I  G  I  K>

       250        260        270        280        290        300
AAGAAAAACCCAAAACTTCATTTGTGTGCACTTACTGCAGTAAAGCTTTCAGGGACAGCT
K  E  K  P  K  T  S  F  V  C  T  Y  C  S  K  A  F  R  D  S>

       310        320        330        340        350        360
ATCACCTGAGGCGCCACGAATCCTGCCACACAGGGATCAAGTTGGTGTCCCGGCCAAAGA
Y  H  L  R  R  H  E  S  C  H  T  G  I  K  L  V  S  R  P  K>

       370        380        390        400        410        420
AAACCCCCACCACGGTGGTTCCCCTTATCTCTACCATCGCTGGGGACAGCAGCCGAACTT
K  T  P  T  T  V  V  P  L  I  S  T  I  A  G  D  S  S  R  T>

       430        440        450        460        470        480
CGTTGGTCTCGACCATTGCAGGCATCTTGTCAACAGTCACTACATCTTCCTCGGGCACCA
S  L  V  S  T  I  A  G  I  L  S  T  V  T  T  S  S  S  G  T>

       490        500        510        520        530        540
ACCCCAGTAGCAGTGCCAGCACCACAGCTATGCCAGTGACCCAGTCTGTCAAGAAACCCA
N  P  S  S  S  A  S  T  T  A  M  P  V  T  Q  S  V  K  K  P>

       550        560        570        580        590        600
GTAAGCCTGTCAAGAAGAACCATGCTTGTGAGATGTGTGGGAAGGCCTTCCGAGATGTGT
S  K  P  V  K  K  N  H  A  C  E  M  C  G  K  A  F  R  D  V>

       610        620        630        640        650        660
ACCATCTCAATCGACACAAGCTCTCCCATTCAGATGAGAAACCCTTTGAGTGTCCTATTT
Y  H  L  N  R  H  K  L  S  H  S  D  E  K  P  F  E  C  P  I>

       670        680        690        700        710        720
GTAATCAGCGCTTCAAGAGGAAGGACCGGATGACTTACCATGTGAGGTCTCATGAAGGAG
C  N  Q  R  F  K  R  K  D  R  M  T  Y  H  V  R  S  H  E  G>

        730        740        750        760        770        780
GCATCACCAAACCCTATACTTGCAGTGTTTGTGGGAAAGGCTTCTCAAGGCCTGACCACT
G  I  T  K  P  Y  T  C  S  V  C  G  K  G  F  S  R  P  D  H>
```

FIGURE 2 (CONT)

```
       790       800       810       820       830       840
TAAGCTGTCATGTAAAACATGTCCATTCAACAGAAAGACCCTTCAAATGCCAAACGTGCA
L  S  C  H  V  K  H  V  H  S  T  E  R  P  F  K  C  Q  T  C>

       850       860       870       880       890       900
CTGCTGCCTTTGCCACCAAAGACAGACTGCGGACACACATGGTGCGCCATGAAGGCAAGG
T  A  A  F  A  T  K  D  R  L  R  T  H  M  V  R  H  E  G  K>

       910       920       930       940       950       960
TATCATGTAACATCTGTGGGAAGCTCCTGAGTGCAGCATACATCACCAGCCACTTAAAGA
V  S  C  N  I  C  G  K  L  L  S  A  A  Y  I  T  S  H  L  K>

       970       980       990      1000      1010      1020
CTCATGGGCAGAGCCAAAGTATCAACTGTAATACATGTAAACAAGGCATCAGTAAAACAT
T  H  G  Q  S  Q  S  I  N  C  N  T  C  K  Q  G  I  S  K  T>

      1030      1040      1050      1060      1070      1080
GCATGAGTGAAGAGACCAGTAACCAAAAGCAGCAGCAGCAGCAGCAGCAGCAACAACAAC
C  M  S  E  E  T  S  N  Q  K  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q>

      1090      1100      1110      1120      1130      1140
AACAACAACATGTGACAAGCTGGCCAGGGAAGCAAGTAGAAACACTCAGACTGTGGGAAG
Q  Q  Q  H  V  T  S  W  P  G  K  Q  V  E  T  L  R  L  W  E>

      1150      1160      1170      1180      1190      1200
AAGCTGTTAAAGCAAGGAAGAAAGAAGCTGCTAACCTGTGCCAAACCTCCACGGCTGCTA
E  A  V  K  A  R  K  K  E  A  A  N  L  C  Q  T  S  T  A  A>

      1210      1220      1230      1240      1250      1260
CGACACCTGTGACTCTCACTACTCCATTCAGTATAACATCCTCTGTGTCGTCTGAGACTA
T  T  P  V  T  L  T  T  P  F  S  I  T  S  S  V  S  S  E  T>

      1270      1280      1290      1300      1310      1320
TGTCAAACCCAGTCACAGTGGCAGCTGCAATGAGCATGAGAAGTCCAGTAAATGTTTCAA
M  S  N  P  V  T  V  A  A  A  M  S  M  R  S  P  V  N  V  S>

      1330      1340      1350      1360      1370      1380
GTGCAGTTAACATAACCAGCCCAATGAACATAGGGCATCCTGTAACTATAACCAGTCCAT
S  A  V  N  I  T  S  P  M  N  I  G  H  P  V  T  I  T  S  P>

      1390      1400      1410      1420      1430      1440
TATCCATGACCTCTCCTTTAACACTCACTACCCCAGTCAACCTCCCCACCCCCGTCACTG
L  S  M  T  S  P  L  T  L  T  T  P  V  N  L  P  T  P  V  T>

      1450      1460      1470      1480      1490      1500
CCCCAGTGAATATAGCACACCCTGTCACCATCACATCTCCAATGAATCTACCCACACCTA
A  P  V  N  I  A  H  P  V  T  I  T  S  P  M  N  L  P  T  P>

      1510      1520      1530      1540      1550      1560
TGACATTAGCCGCCCCTCTCAATATAGCAATGAGACCTGTAGAGAGCATGCCTTTCTTGC
M  T  L  A  A  P  L  N  I  A  M  R  P  V  E  S  M  P  F  L>
```

FIGURE 2 (cont)

```
       1570      1580      1590      1600      1610      1620
CCCAAGCTTTGCCTACATCACCGCCTTGGTAAACAGTATTATAAAATCAAAATATGGGTA
P  Q  A  L  P  T  S  P  P  W  *>

       1630      1640      1650      1660      1670      1680
AAAGTAAATATTTACCAGCAACTTAACTTTTAGTTGATTAAAGCAAAAAGTAAACCATGA

       1690      1700      1710      1720      1730      1740
AATTGGGAGATTTTATTACATTAGTTAATAAGAGTGTGGTAGCATTTTTCTCCAATTTGG

       1750      1760      1770      1780      1790      1800
CTGGGATTATTCAAAGTAGGGTGTGTATGTAACTTATCACTGGACCACTTTAGTTTAATC

       1810      1820      1830      1840      1850      1860
AGAAATTCCTTTTAGCTGACAACATTGCTTAAACAGGATAGTAGTTGGCAAGATGAAATG

       1870      1880      1890      1900      1910      1920
CCAGAATTAAAACCAATCATAAGTAGAACCCACTTCAAAATAAAAAAACAGCATTACTAT

       1930      1940      1950      1960      1970      1980
TTCTAATCCCAAGGAATCACTTTATTGTAAACACTAGCAGAACTCTTCTCCCTATACAAG

       1990      2000      2010      2020      2030      2040
GTGGATGGCTGATTTTAACCTGAAATTTTAAATCCACAGATTGAGAGCTAGTGTAGAATT

       2050      2060      2070      2080      2090      2100
GTCTGTGTTTATTGTTTTTATGAGTAAATACATGCATTGTCATAATAAAATGCATTTCAG

       2110      2120      2130      2140      2150      2160
AGAATATGCATTTTACCTTTGGGAATATGTTAATTTCAGGCAGCATTCCCTATGGGAAAG

       2170      2180      2190      2200      2210      2220
GTGATACCAGCTCTGATATGCAAAGCATATGATAATTTATCATTCTAACTTCAACGTATA

       2230      2240      2250      2260      2270      2280
ATAGGGATTGTGACCTGATATTTGGAGATGTAAATATTGCTCAGCATATTAATCCCGATG

       2290      2300
GAATATAGCATTGTAGTTGACTTTTT
```

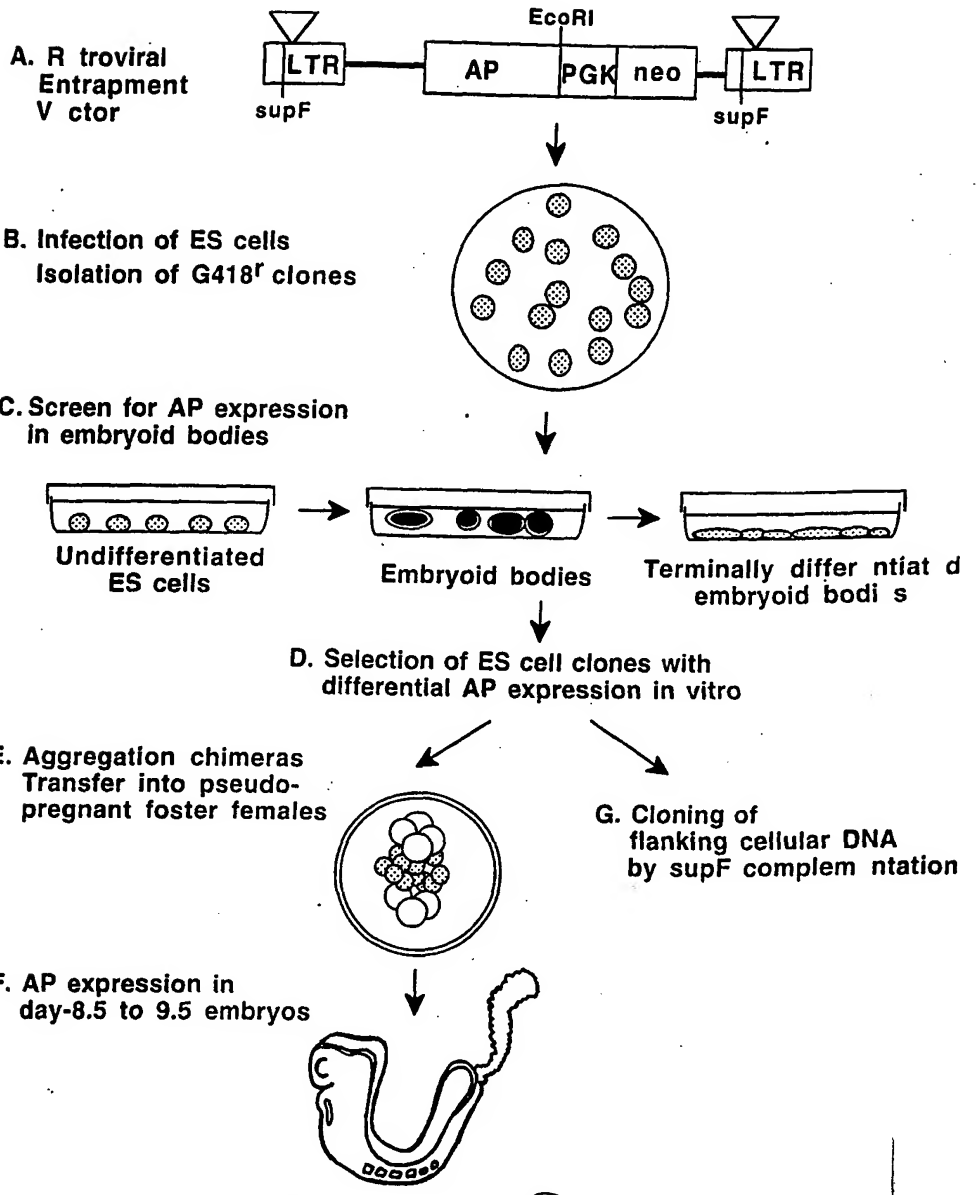


FIGURE 3.

3200 (Sheet 6 of 20)

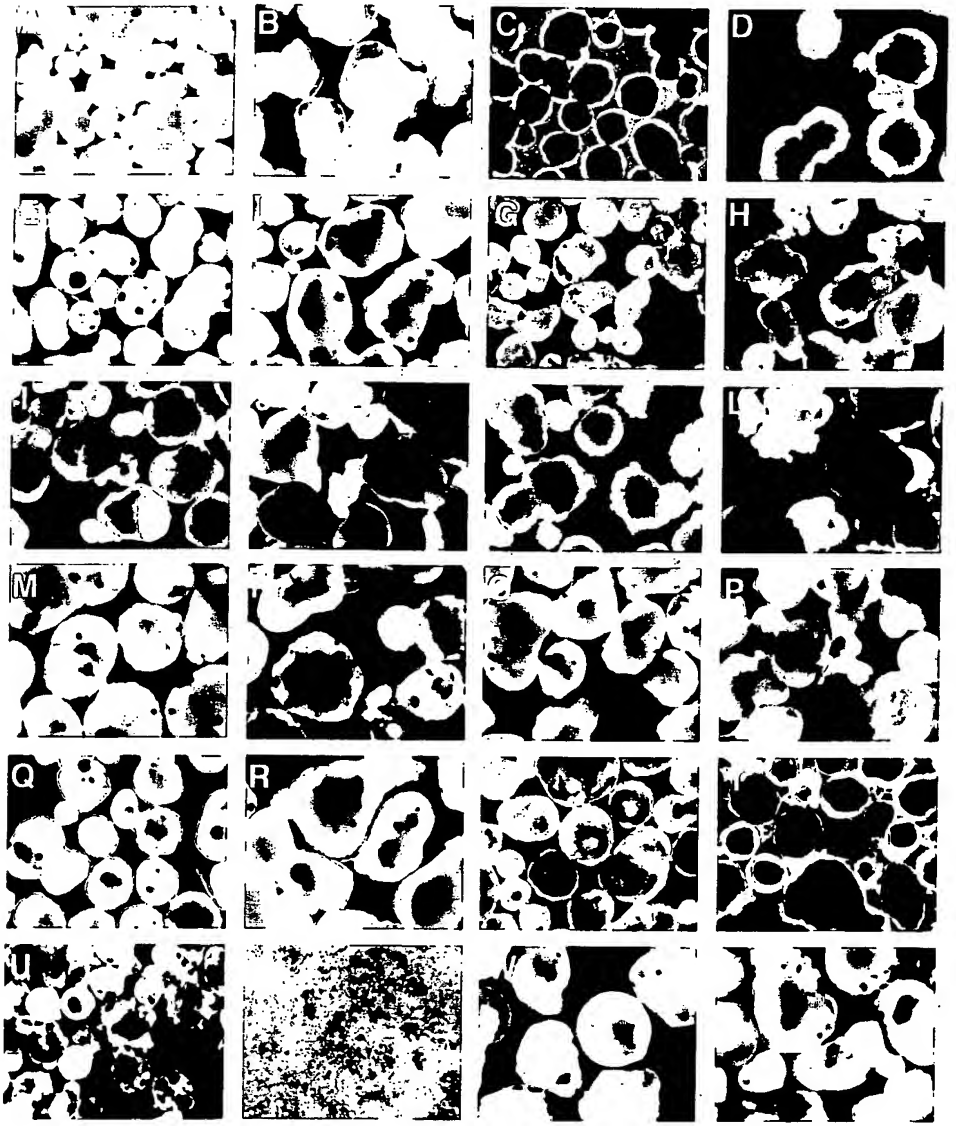


FIGURE 4.

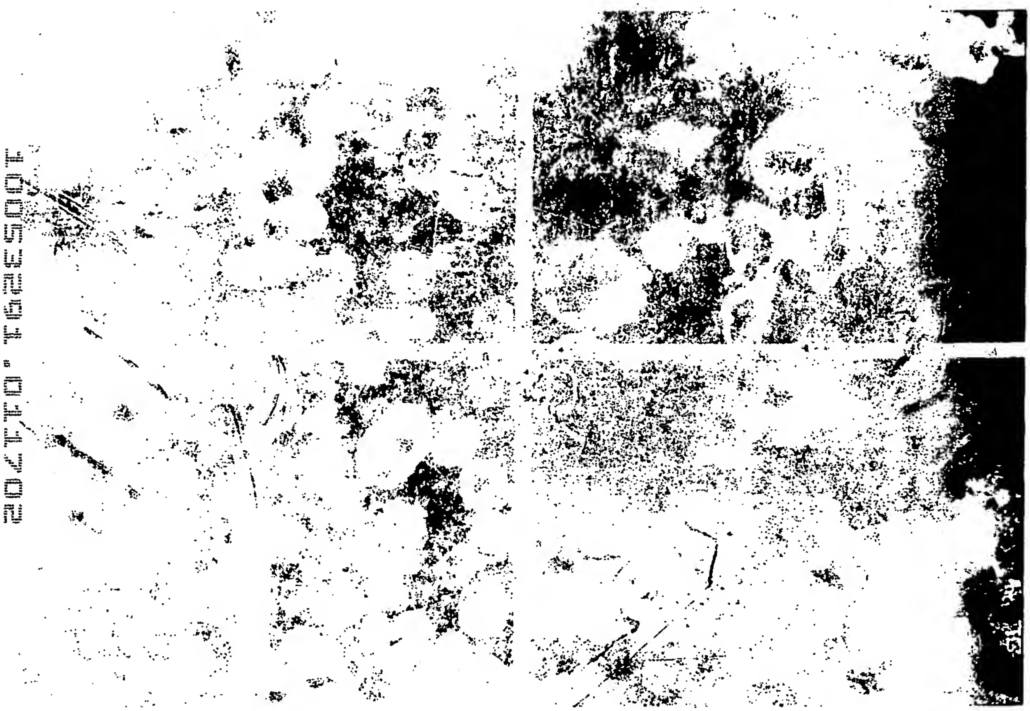
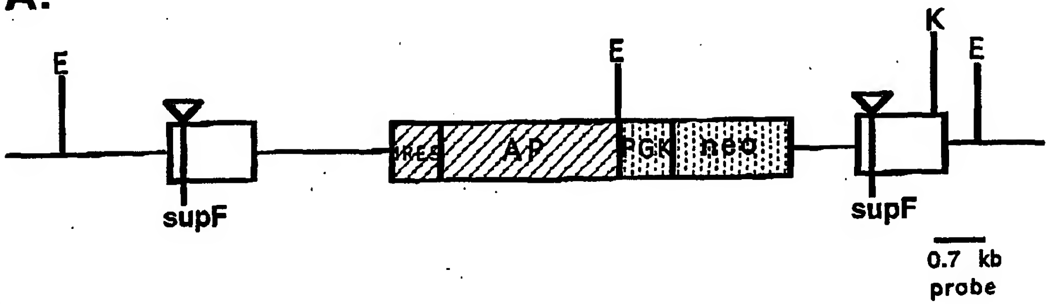


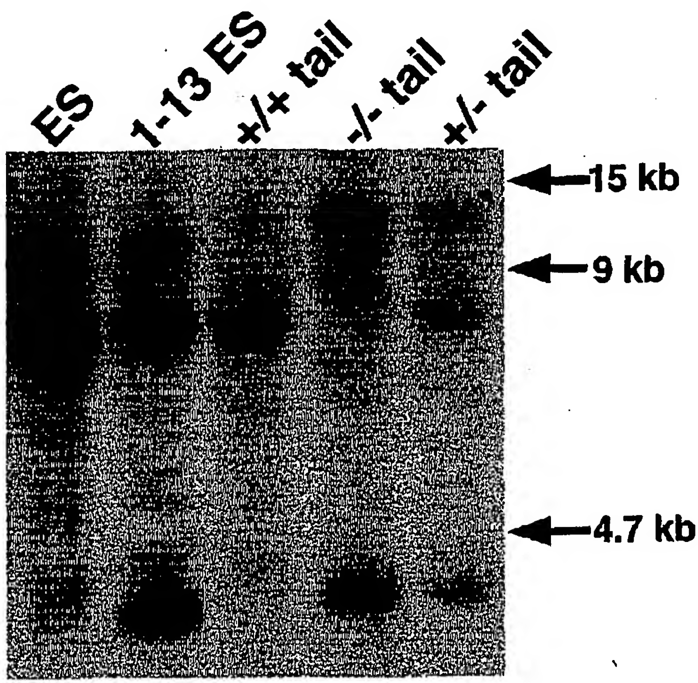
FIGURE 5.

FIGURE 6.

A:



B:



Alignment of Vezf1/mPur1:

```
Vezf1    168  KPVKKNHACEMCGKAFRDVYHLNRHKLSHSDEKPFECPICNQRFKRKDRMTYHVRSHEGGITKPYTCSVCGKGFSRPDHLSCHVKHVHSTERPFKCQ  264
mPur1    275  KRIRKNHACEMCGKAFRDVYHLNRHKLSHSDEKPYQCPVCQQRFKRKDRMSYHVRSHDGAVHKPYNCSHCGKSFSRPDHLNSHVRQVHSTERPFKCE  372

Vezf1    265  TCTAAFATKDRLRTHMVRHEGKVSCNICGKLLSAAYITSHLKTHGQSQSINCNTCKQGISKTCMSEETSNQKQQQQQQQQQQQQQQQHVTSWPGKQ  360
mPur1    373  KCEAAFATKDRLRAHTVRHEEKVPCHVCGKMLSSAYISDHMKVHSQGPHHVCELCNKGTGEVCPMAAAAAAAAAAAAAAVVAAPPTAVGSLSGAGEV  469
```

FIGURE 7.

3/2004 (sheet 9 of 9)

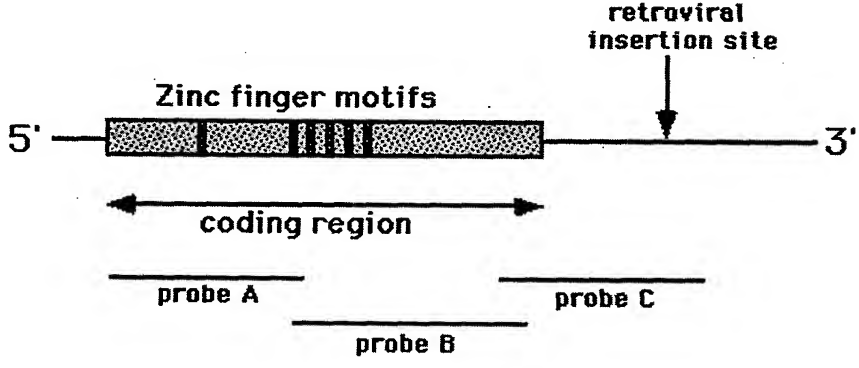


FIGURE 8.

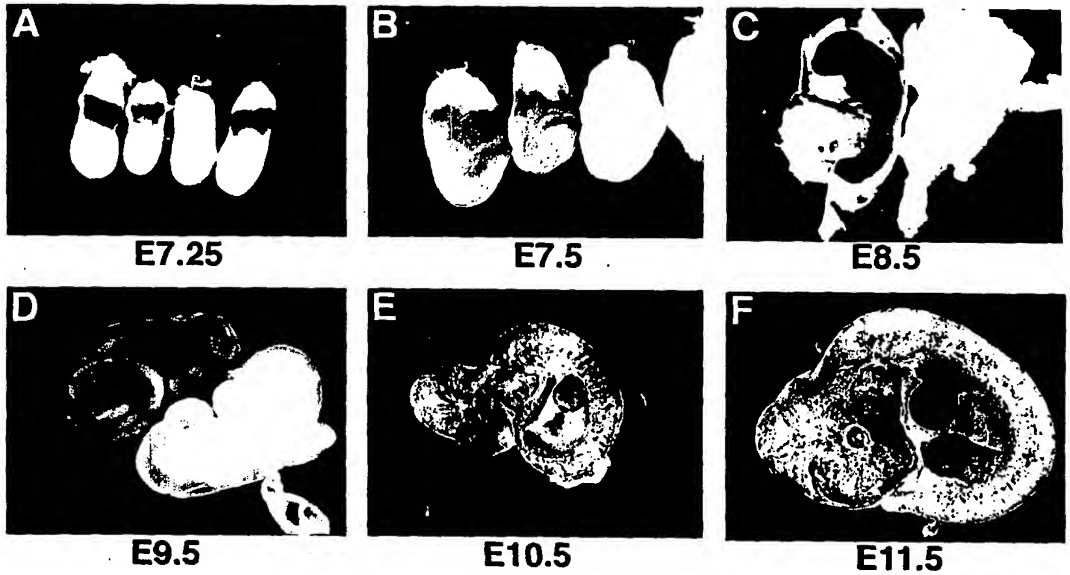


FIGURE 9

3/00 (Sheet 11 of 20)

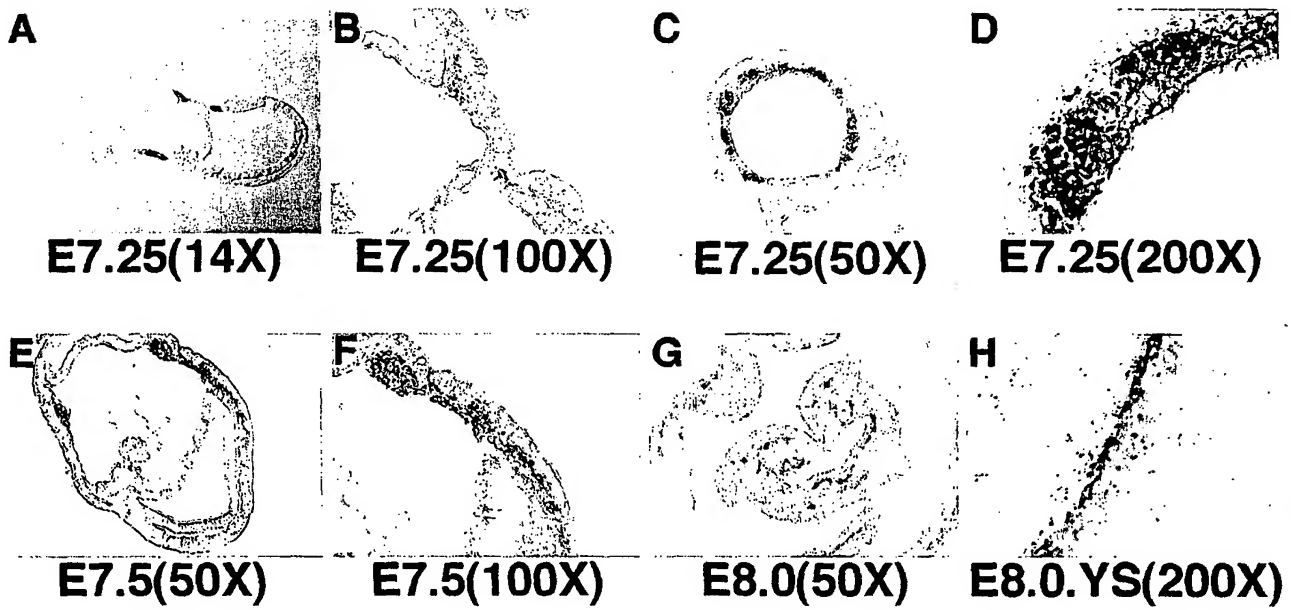


FIGURE 10.

3/9 (sheet 10/9)

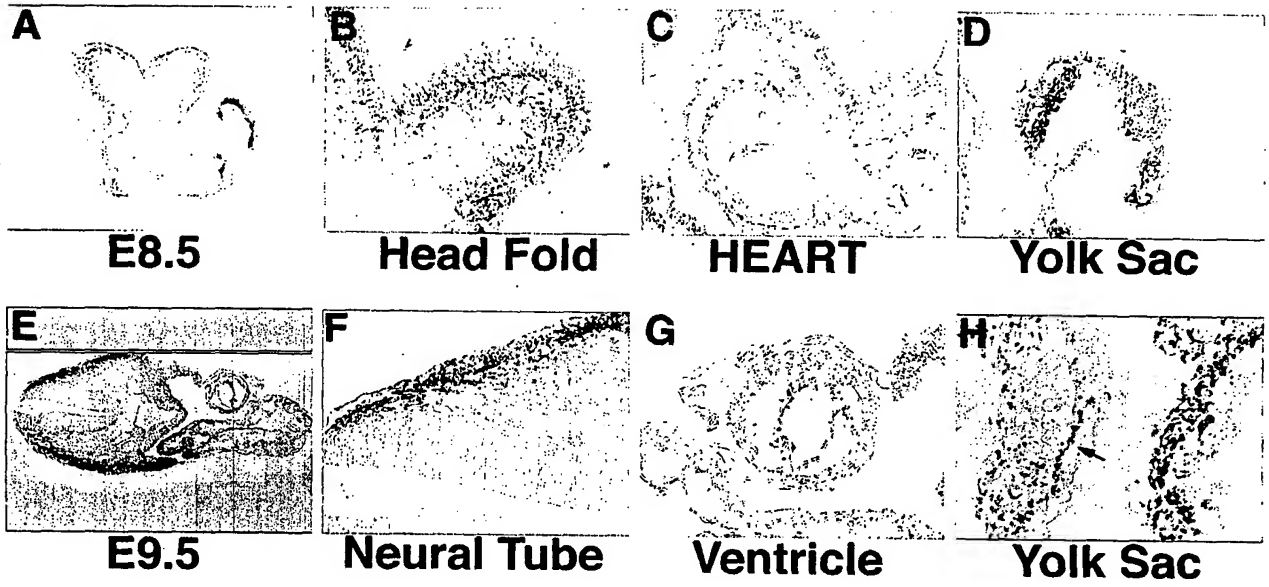


FIGURE 11.

Sub 0 (Sheet 13 of 30)

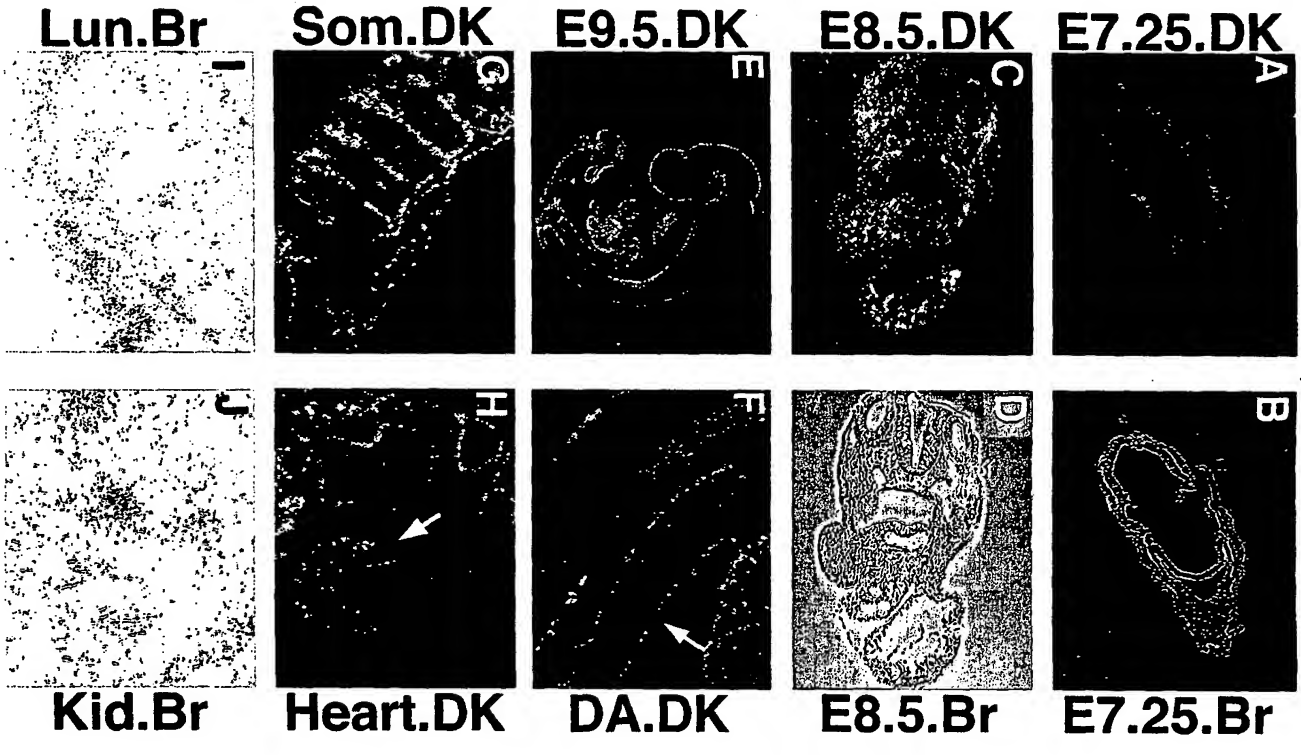


FIGURE 12.

31.00 (sheet 14 of 29)

3/20 (Sheet 15 of 20).

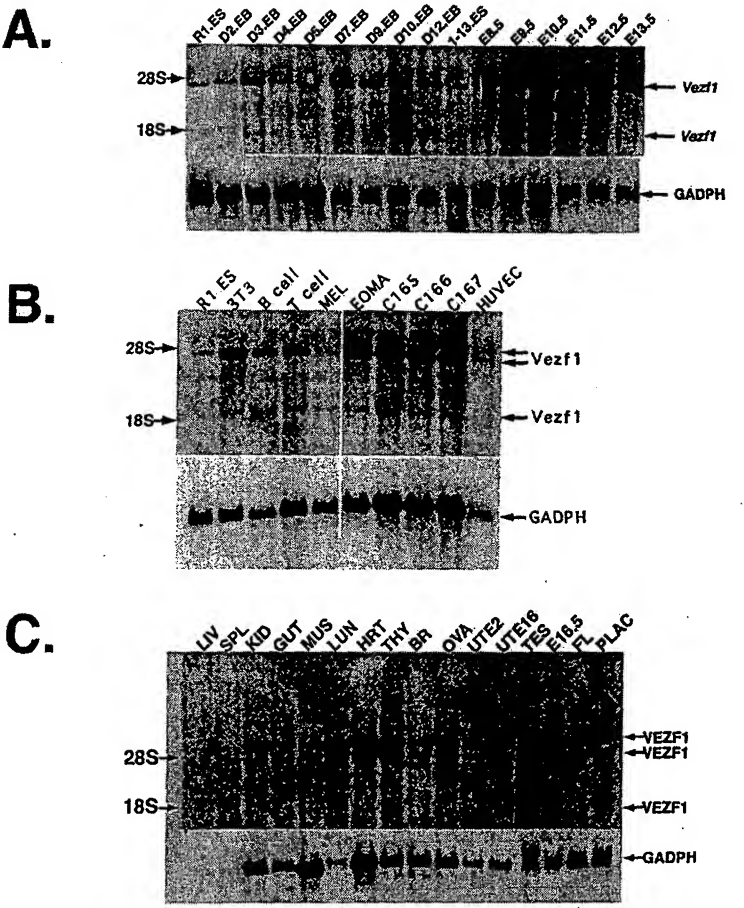


FIGURE 13.

Sheet 10 (Sheet 10 of 30)

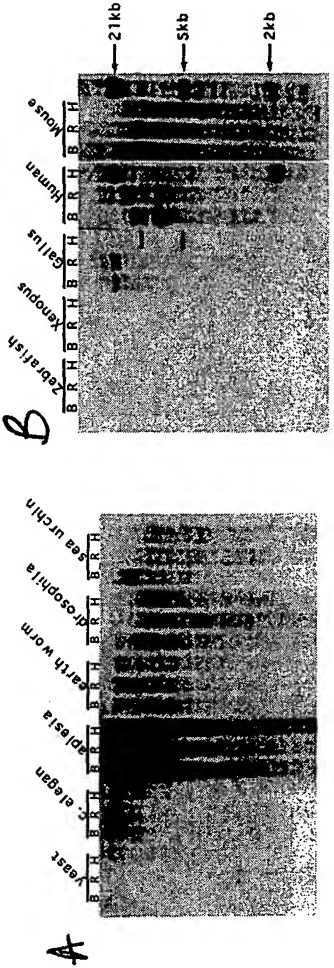
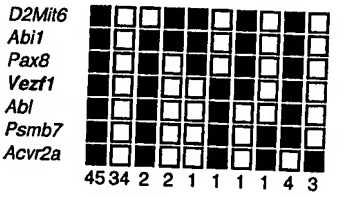


FIGURE 14.

5 200 (sheet 17 of 20)

A: Jackson BSS Chromosome 2



B: Jackson BSS Chromosome 2

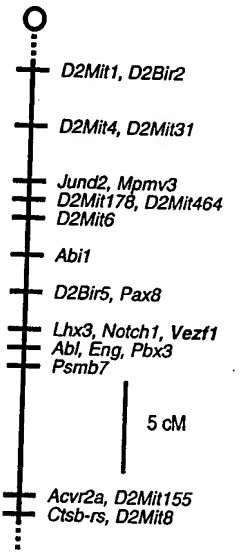
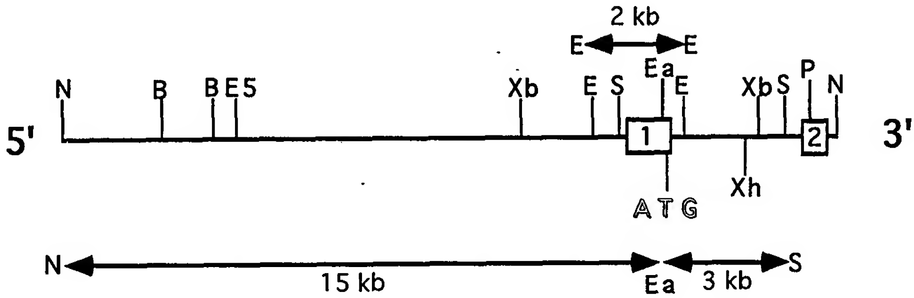


FIGURE 15.

Restriction Enzyme Map of a 20 kb Genomic DNA of the Vezf1 Gene



BamHI (B), EcoRI (E), EcoRV (E5), EagI (Ea), NotI (N), PatI (P), SacI (S), XbaI (Xb), and XhoI (Xh).

— Intronic sequence;

[1] Exon 1

[2] Exon 2

FIGURE 1G.

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Vezf1 EXPRESSION VECTORS

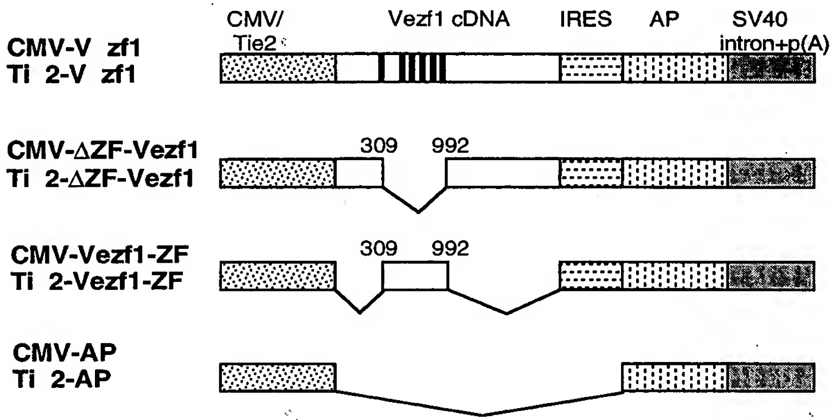

FIGURE 17.

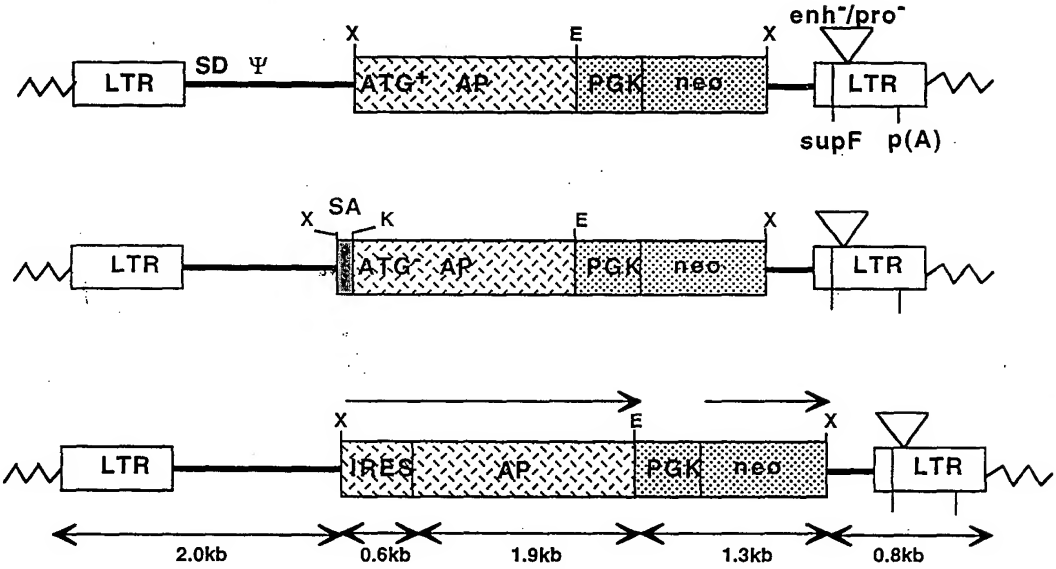

FIGURE 18.

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